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(12) **EUROPEAN PATENT SPECIFICATION**

(45) Date of publication and mention  
of the grant of the patent:  
**25.11.1998 Bulletin 1998/48**

(51) Int Cl.<sup>6</sup>: **C12N 15/62, C12N 15/63,  
C07K 14/52, C12N 5/10,  
C12N 1/21, C12N 1/15,  
A61K 38/19, C07K 16/24**

(21) Application number: **92918688.0**

(22) Date of filing: **24.08.1992**

(86) International application number:  
**PCT/US92/07112**

(87) International publication number:  
**WO 93/05169 (18.03.1993 Gazette 1993/08)**

(54) **HYBRID CYTOKINES**  
**HYBRIDE CYTOKINE**  
**CYTOKINES HYBRIDES**

(84) Designated Contracting States:  
**AT BE CH DE DK ES FR GB GR IE IT LI LU MC NL  
SE**

(30) Priority: **30.08.1991 US 753178**

(43) Date of publication of application:  
**15.06.1994 Bulletin 1994/24**

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Remarks:  
The file contains technical information submitted  
after the application was filed and not included in this  
specification

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EP 0 601 043 B1

**Description****Technical Field**

5 The invention relates to the field of cell proliferation and differentiation and to factors which regulate the composition of the blood and the viability of other tissues. More specifically, the invention concerns hybrid cytokines which have unique physiological properties derived from the cytokine family members leukemia inhibitory factor (LIF); granulocyte colony stimulating factor (G-CSF); interleukin-6 (IL-6); and oncostatin-M (OSM).

**Background Art**

10 More than two dozen cytokines that regulate blood composition by controlling the growth and differentiation of hematopoietic stem cells have been identified. The interferons, tumor necrosis factor, stem cell factor, the numbered interleukins and the various colony stimulating factors are exemplary of these proteins and glycoproteins. The invention  
15 described below focuses on four closely related cytokines whose structural similarity has been discovered by applicants.

One of these factors, interleukin-6 (IL-6) was originally identified as a B-cell differentiation factor, but has subsequently been shown to induce acute phase proteins in liver cells, to inhibit growth of certain myeloid leukemia cell lines and induce their differentiation into macrophage cells, to promote IL-3 dependent colony formation of primitive blast  
20 colony forming cells, to cause differentiation of neuronal cells, to enhance keratinocyte and mesangial cell growth, to promote the maturation of megakaryocytes, and to induce the proliferation and differentiation of T cells. *In vivo*, IL-6 increases the hematopoietic cell count of the erythroid, myeloid, and thrombocytic lineages. Other former names for IL-6 are beta2-interferon, B-cell stimulatory factor-2, hybridoma/plasmacytoma growth factor, and monocyte granulocyte inducer type 2. The spectrum of activities attributable to IL-6 indicates that it is useful in tumor inhibition, bone  
25 remodeling, kidney development, and T- and B-cell proliferation and stimulation.

Leukemia inhibitory factor (LIF) has been demonstrated to inhibit the growth of certain myeloid leukemia cells and to induce their differentiation into macrophage cells; to enhance interleukin-3 dependent colony formation of primitive blast cells; to promote megakaryocyte growth and differentiation; to induce neuronal differentiation; to stimulate the production of acute phase proteins and hepatocytes (all properties it shares with IL-6) and to inhibit the differentiation  
30 of embryonic stem cells and kidney cells and to induce bone resorption.

Oncostatin-M (OSM) is known to be a tumor inhibitor for melanoma and certain carcinoma cells and inhibits the growth of human A375 melanoma cells but not normal human fibroblasts. It is also an inhibitor of the growth of M1 myeloid leukemic cells and induces their differentiation into macrophage-like cells as well as stimulating megakaryocyte production in the spleen. This factor was first isolated from conditioned medium of U937 human histolytic leukemia  
35 cells that had been induced with phorbol myristate acetate (PMA) and is also present in the supernatants of activated human T-cells.

Granulocyte colony stimulating factor (G-CSF) stimulates neutrophil proliferation and differentiation and induces the differentiation of M1 murine myeloid leukemic cells into macrophage-like cells as well as enhancing interleukin-3 dependent colony formation of primitive blast cells. It appears to have little effect on the hematopoietic cell lineages of  
40 megakaryocytes or platelets but enhances cytosine arabinoside-mediated cytotoxicity in human myeloid leukemia cells.

The reported biological activities of the foregoing cytokine family members is summarized in the following table:

**Table 1**  
**Reported Biological Activities of Cytokine Family Members**

	<u>LIF</u>	<u>OSM</u>	<u>G-CSF</u>	<u>IL-6</u>
Endothelial Cell Proliferation	NR	+	NR	NR
Tumor Inhibition	+	+	NR	+
Embryonic Stem Cell Maintenance	+	+	NR	NR
Hematopoietic Leukemic Cell Differentiation	+	+	+	+
Melanoma Cell Inhibition	-	+	-	+
Neutrophil Proliferation/Stimulation	NR	NR	+	+
Myoblast Proliferation	+	NR	NR	NR
Bone Remodeling	+	NR	NR	+
Kidney Development	+	NR	NR	NR
Neuronal Differentiation	+	NR	NR	+
Hepatocyte Stimulation	+	NR	NR	+
Megakaryocyte Augmentation	+	NR	-	+
T-Cell Proliferation	NR	NR	NR	+
Keratinocyte Proliferation	NR	NR	NR	+
B-Cell Proliferation/Stimulation	NR	NR	NR	+
Binding to Human Placental Cell Receptor	+	+	-	-

These data were obtained from multiple assay systems and few direct comparisons of the growth factors have been made. The table lists several biological systems in which one of the four growth factors shows activity, while the role of other family members is not yet known. NR=not reported.

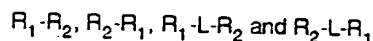
As shown in the foregoing table, the four related factors that are the subject of the present invention do not display identical activity patterns. Although a number of characteristics have not yet been reported for each of these factors, it is clear that at least one difference in activity spectrum exists between any two of them. For example, OSM and IL-

6 inhibit the growth of melanoma cells; LIF and G-CSF do not. However, LIF and G-CSF differ in that LIF is capable of augmenting megakaryocytes; G-CSF is not. OSM binds to human placental cell receptor; IL-6 does not.

While there have been excellent clinical successes, especially with the use of G-CSF in enhancing the health of the immune system and white blood cell replacement in patients with depleted lymphocyte populations, such as patients undergoing radiation or chemotherapy, no ideal pharmaceutical which has the desired effects, free of complications, has been discovered. Clearly this is not surprising, since normally the composition of the blood is regulated by controlling the differentiation of cells originating in the bone marrow through the interaction of a multiplicity of indigenous factors whose levels are in turn presumably controlled by mechanisms not yet understood. Thus, it is desirable to augment the repertoire of available therapeutic agents which participate in the control of blood composition. The present invention augments this repertoire by providing hybrid cytokines with unique properties characteristic of these previously unavailable therapeutic agents.

Williams et al., *Int. J. Cell Cloning* 9 (1991), 542-547 disclose the creation of a granulocyte-macrophage colony-stimulating factor (GM-CSF)/interleukin 3 (IL-3) fusion protein; see page 542, Abstract, lines 2 and 3. This fusion protein (PIXY321) is a combination or fusion of the two complete native cytokines GM-CSF and IL-3 which results in a recombinant polypeptide with at least eight helical regions.

WO 91/02754 discloses the construction of fusion proteins comprising GM-CSF and IL-3; see page 1, lines 11 and 12. The fusion proteins include constructs in which the C-terminal portion of GM-CSF is fused to the N-terminal portion of IL-3, and also constructs in which the C-terminal portion of IL-3 is fused to the N-terminal portion of GM-CSF. Specifically, the fusion proteins have the formula selected from the group consisting of



wherein  $R_1$  is GM-CSF;  $R_2$  is IL-3; and L is a linker peptide sequence.\*

Williams and Park, *Cancer* 67 (1991), 2705-2707 disclose the production of a GM-CSF/IL-3 fusion protein (pIXY 321) in a yeast expression host and the hematopoietic effects of this fusion protein; see page 2705, Abstract, lines 4 and 5 and Headline. To produce the fusion protein an expression vector was constructed containing sequences encoding (5') GM-CSF, followed by sequences encoding a flexible synthetic linker sequence and the coding region of IL-3 (-3'); see page 2705, right column, second para, lines 3 to 6.

#### Disclosure of the Invention

The invention is directed to therapeutic hybrid cytokines which are composed of portions of the closely related cytokines leukemia inhibitory factor (LIF), granulocyte-colony stimulating factor (G-CSF), interleukin-6 (IL-6) and oncostatin-M (OSM). These cytokines have a high degree of sequence homology (as well as a similar genetic organization). It is disclosed in the art that IL-6 and G-CSF are comprised of four  $\alpha$ -helical regions; applicants herein have deduced that LIF and OSM also are comprised of four  $\alpha$ -helical regions organized in a similar manner. In each case, the four helical regions are linked by non- $\alpha$  helical sequences of about 5-100 amino acids, and in some cases the  $\alpha$ -helices are maintained in the proper conformation and geometry with respect to each other through disulfide bridges. The hybrid cytokines of the invention also contain four  $\alpha$ -helical regions, at least two of which are derived from the corresponding  $\alpha$ -helical regions of different members of this group. The linking amino acid sequences preferably are also derived from the four factors described herein.

Thus, in one aspect, the invention is directed to a hybrid cytokine comprising a first, second, third and fourth  $\alpha$ -helical region. Each of these regions is derived from the corresponding  $\alpha$ -helical region of LIF, G-CSF, IL-6, or OSM. At least one of these regions is derived from a different factor of this group than at least one other.

In additional aspects, the invention is directed to DNA sequences encoding the hybrid cytokines, to expression systems capable of expressing these DNAs, to host cells transformed with these expression systems and to methods to produce the hybrid cytokines recombinantly. In still other aspects, the invention is directed to pharmaceutical compositions containing the hybrid cytokines of the inventions and to methods to effect therapies using these compositions. In addition, the invention is directed to antibodies or fragments specifically immunoreactive with these hybrid cytokines.

#### Brief Description of the Drawings

Figure 1 shows the complete amino acid sequences of LIF, OSM, G-CSF and IL-6 from various species—human, murine, and simian (SEQ ID NO:1), (SEQ ID NO:2), (SEQ ID NO:3), (SEQ ID NO:4), (SEQ ID NO:5), (SEQ ID NO:6), (SEQ ID NO:7), and (SEQ ID NO:8).

Figure 2 shows the three-dimensional organization deduced for the OSM, LIF, G-CSF and IL-6 factors used to construct the hybrids of the invention. Also shown in this figure is the three-dimensional organization of growth hormone

which has been confirmed by X-ray crystallography.

#### Modes of Carrying Out the Invention

The availability of the DNA sequences encoding the four factors used as portions of the hybrid, LIF, G-CSF, IL-6 and OSM, makes possible the construction of recombinant DNA encoding the desired hybrid cytokine. As shown in Figure 1, the complete amino acid sequence (and corresponding DNA sequence) is available with respect to human, murine and simian forms of these cytokines. The close homology shown among species also makes possible the retrieval of the corresponding DNAs from additional species producing such cytokines, such as feline, canine, bovine, avian, and other vertebrate species. Natural allelic variants may also be retrieved. Accordingly, the hybrid cytokine encoding DNA can be constructed using DNAs of species origin appropriate for the particular hybrid desired.

The DNA encoding the amino acid sequences of the hybrid cytokines will be "derived from" the DNA encoding the relevant portions of the native cytokine. By "derived from" is meant that the amino acid sequence encoded is the same as that of the native protein--either that shown in Figure 1, a naturally-occurring allelic variant, a mutant shown to bind to the receptor of the relevant cytokine in standard *in vitro* assays, or that of an additional species obtainable by using the known species DNA as probes. "Derived from" does not imply any physical derivation. Typically, the portions of the protein sequence "derived from" the native cytokines are, in fact, prepared using either genomic or cDNA, synthesized DNA, or combinations of these. Of course, any DNA encoding the desired sequence can be used, not necessarily that DNA sequence which occurs natively. "Derived from," thus, has no implications that the physical embodiment of either the DNA or the protein portion is used in the hybrids of the invention, but that the information provided by the native sequences is used in the construction of suitable DNA and protein.

Exemplary amino acid sequences for the relevant cytokines of various species are shown in Figure 1. The hybrid cytokines of the invention derive amino acid sequences from at least two of the four related factors--leukemia inhibitory factor (LIF), granulocyte-colony stimulating factor (G-CSF), interleukin-6 (IL-6), and oncostatin-M (OSM). The amino acid sequences of each of these factors in human and other species is known, and the encoding genes have been cloned. Human and murine genes encoding LIF are reported by Moreau, J.F., et al., *Nature* (1988) 336:690-692; and by Simpson, R.J., et al., *Eur J Biochem* (1988) 175:541-547; for human and murine G-CSF by Nagata, S., et al., *Embo J* (1986) 5:575-581, and by Tsuchiya, M., et al., *Proc Natl Acad Sci USA* (1986) 83:7633-7637; for human and murine IL-6 by Yasukawa, K., et al., *Embo J* (1987) 6:2939-2945, and by Tanabe, O., et al., *J Immunol* (1988) 141:3875-3881; and for human OSM by Malik, N., et al., *Mol Cell Biol* (1989) 9:2847-2853; and for simian OSM (unpublished results).

Alignments for the amino acid sequences of these proteins are shown in Figure 1. The homology correlations, alignment, and secondary structure determinations were conducted using a number of software packages including PatMat software (Henikoff, S., et al., *Methods Enzymol* (1990) 183:111-132; GenPro software (Riverside Scientific, Seattle, WA)); P/C Gene Software, Intelligenetics, Inc. (Mountain View, CA); Scor Edit from J. Durand (Seattle, WA); Motif Program (Smith, H.O., *Proc Natl Acad Sci USA* (1990) 87:826-830) as implemented in the Protomat/Motif J software from S. Henikoff (Seattle, WA).

Application and interpretation of these programs also led to a prediction of secondary structure for the four factors which comprise the cytokines of the invention.

The results of this work are shown in Figure 2. As shown in Figure 2, each of LIF, G-CSF, IL-6, and OSM contain four  $\alpha$ -helical regions numbered I-IV. The various factors also show disulfide bridges; OSM and LIF having similar locations for the disulfides; as shown OSM and LIF show similar genetic patterns; G-CSF and IL-6 also show similar patterns with each other. The disulfide bond linking the fourth  $\alpha$ -helical region and the linking region between the first and second  $\alpha$ -helices predicted in LIF and shown to be present in OSM is also found in the structure of growth hormone. In human OSM, the  $\alpha$ -helical region I extends approximately from amino acid 11-32;  $\alpha$ -helical region II from 78-99;  $\alpha$ -helical region III from 105-131; and  $\alpha$ -helical region IV from 157-184. The locations of the various regions of  $\alpha$ -helices for the human forms in these four factors are shown in Table 2.

Table 2

Factor	Region	I	II	III	IV
OSM		11-32	78-99	105-131	157-184
LIF		19-46	72-97	108-133	154-180
G-CSF		12-24, 45-56	68-93	104-127	139-173
IL-6		24-41, 54-63	79-102	110-136	147-183

As implied in the table, the various helical regions in each case will be linked by nonhelical peptide sequences designated herein "linking sequences." Thus, for OSM, for example, linking sequence I/II extends from residue 33-77;

linking region II/III from position 100-104; and linking region III/IV from position 132-156. In G-CSF and IL-6, the  $\alpha$ -helical region I is divided into two portions separated by a nonhelical portion in each case. As shown, some of the linking regions, such as OSM linking region II/III are quite short—in this case, only about 5 amino acids. In other cases, an extended linking region is found.

The hybrid cytokines of the invention contain four helical regions each derived from the "corresponding" helical region in one of the four factors described above. As used herein, derived from the "corresponding"  $\alpha$ -helical region means that the first  $\alpha$ -helical region (I) of the hybrid cytokine contains the same or substantially identical amino acid sequence as  $\alpha$ -helical region I of either OSM, LIF, G-CSF or IL-6; the second  $\alpha$ -helical region (II) of the hybrid cytokine has the same or substantially identical amino acid sequence as that of  $\alpha$ -helical region II of one of these factors, and so forth. The four  $\alpha$ -helical regions of the hybrid cytokines are connected by additional nonhelical linking regions ranging from about 4 to about 100 amino acids. In addition, each of the helical regions may be interrupted by one or more nonhelical sequences containing about 6-30 amino acids, analogous to the situation for the first helical regions of the native forms of G-CSF and IL-6.

It is preferred that the helical regions in the hybrid be derived from the cytokine characteristic of the species for which the use is intended. Thus, for human therapy, it is preferred that all four of the regions be derived from the human forms of the cytokines. For veterinary use, for example, in dogs, it is preferred that all of the helical regions derive from the dog corresponding regions. However, in view of the homology exhibited among species with respect to these cytokines, it is within the scope of the invention to combine regions derived from various species.

It is also preferred that the nonhelical linking regions be derived from the corresponding linking regions in the native cytokines. Thus, it is preferred that linking region I/II in the hybrid be derived from linking region I/II of one of the G-CSF, OSM, LIF and IL-6. Derivation from the species for which use is intended is also preferred. However, included within the scope of the invention are hybrid molecules which have arbitrarily chosen linking regions selected to keep the conformation of the three-dimensional molecules similar to those of the native cytokines.

In preferred embodiments, either helical regions I, II, and III are derived from the same factor and IV from a different factor or, conversely, regions II, III and IV are from the same factor and region I is from a different one. In general, it is preferred that regions II and III derive from the same source.

Also preferred are embodiments wherein the relative polarity orientation of regions I-IV is undisturbed from a natural pattern, in particular, regions I and IV with respect to each other. It will be noted that in all four factors the N $\rightarrow$ C directions of regions I and IV are opposite. Similarly, the N $\rightarrow$ C orientations of regions II and III are of opposite polarity. In OSM and LIF, the lengths of the linking region I/II and of linking region III/IV permit regions I and IV to be oriented N $\rightarrow$ C in the same orientation as regions II and III, respectively. The short segments in the linking regions I/II and III/IV in G-CSF and IL-6 force regions I and II and III and IV to be in opposite orientations N $\rightarrow$ C, respectively. However, the "double negative" for G-CSF and IL-6 results in the same relative orientations with respect to regions I and IV in G-CSF and IL-6 as is the case in OSM and LIF.

Thus, in preferred embodiments, either both of linking regions I/II and III/IV will be of about 20-100 amino acids to allow for the parallel orientation of joined helical regions as in LIF and OSM, or both should be relatively short of less than 20 amino acids to force antiparallel orientation in both cases as in G-CSF and IL-6. Thus, the linking regions should be selected so as to assure antiparallel orientation of regions I and IV in all cases.

Also particularly preferred embodiments are those wherein the first and second  $\alpha$ -helical regions are derived from G-CSF or wherein at least one region is derived from IL-6. Particularly preferred embodiments with respect to the origin of the  $\alpha$ -helical regions are as follows, wherein the  $\alpha$ -helical regions I-IV are ordered as shown, and wherein G represents G-CSF; L represents LIF; I represents IL-6; and O represents OSM: GGGL; OOOI; LLLI; IIII; GGGO; OOOO; LLLO; IIIG; GGGL; OOOI; LLLI; IIII; IGGG; IOOO; ILLL; OIII; OGGG; GOOO; OLLL; GIII; LGGG; LOOO; GLLL; LIII; GGLL; GGII; GGGO; GILO; LOGI; LLI; LLGG; IIGG; and OOGG.

The  $\alpha$ -helical regions shown are, then, linked through nonhelical linking regions of 4-100 amino acids, preferably derived from the linking regions of the native cytokines. Thus, preferred embodiments of the foregoing are those wherein the linking regions are as indicated derived from the corresponding linking region of the native cytokine. In the abbreviations used in the following, g represents a linking region from G-CSF; l represents a linking region from LIF; i represents a linking region from IL-6; and o represents a linking region from OSM. In each case, the indicated linking region is derived from the corresponding linking region of the indicated cytokine; thus that shown between  $\alpha$ -helical sequence I and II is derived from the linking region I/II.

Thus, especially preferred are the following: GIGILI; GIGgII; GgGgOgO; GIGiGoI; liGgGgG; GgliLiO; LgOgGgI; LoLlIoI; GgGgGgO; GgGgGgI; OoOoOoG; LLLIIG; GoOoOoO; OgGgGgG; LgGgGgG; GiGgGgI.

As it is believed that the disulfide linkages shown in Figure 2 are helpful in maintaining conformation, choice of the suitable linking region or  $\alpha$  helical region which provides cysteine residues to furnish the appropriate disulfide links are preferred. Alternatively, a cysteine residue may be substituted at the appropriate position in place of one of the residues in the linking or helical region derived from a different source.

Synthesis of the Hybrid Cytokines

The hybrid cytokines, in principle, could be made using standard solid-phase peptide synthesis techniques, in combination with linking technology. However, synthesis of peptides of the appropriate length is laborious and difficult. Conditions would need to be provided subsequent to the synthesis to effect the three-dimensional folding required for the molecules to assume the  $\alpha$ -helical and tertiary conformations shown. A more practical approach to the preparation of the hybrid cytokines of the invention is the recombinant production thereof.

Use of recombinant technology to produce any desired protein is by now well established in the art. The requirements for such recombinant production are well known--the provision of a coding sequence for the desired protein, which coding sequence will be operably linked to additional DNA sequences capable of effecting its expression. It may be desirable to produce the hybrid cytokines as fusion proteins which can be freed from upstream or downstream (or intermediate) regions or to produce them linked to leader sequences capable of effecting the secretion of the desired cytokines into the cell culture medium.

The DNA-based expression system will also contain "control sequences" which are necessary for the transcription and translation of the message. Known components required for expression include promoter systems which may be constitutive or inducible, translational initiation signals, in eucaryotic expression, polyadenylation translation termination sites, and transcription terminating sequences. Host vectors containing these controls which permit desired coding sequences to be operably linked to the required control systems are by now well established in the art, and such vectors operable in a variety of hosts can be found.

Thus, the hybrid cytokines of the invention may be produced in procaryotic cells using appropriate controls, such as the trp or lac promoter, or in eucaryotic host cells which are capable of effecting the post-translational processing that permits that protein to assume the desired three-dimensional conformation. Eucaryotic control systems and host vectors are also well known; including the leu and glycolytic promoters useful in yeast, the viral SV40 and adenovirus promoters in mammalian cells, inducible promoters such as the metallothionein promoter also suitable for mammalian cells, and the baculovirus system which is operable in insect cells. Plant vectors with suitable promoters, such as the nos promoter are also well known.

The hybrid cytokines of the invention can be prepared conveniently in procaryotic as well as eucaryotic hosts since, although generally glycosylated in their native forms, glycosylation is known not to be essential for their activity. Suitable conditions for refolding can also be provided as is understood in the art.

Standard techniques for expression of DNAs encoding any desired protein and techniques and methodologies for culturing the appropriate cells, providing the conditions suitable for expression, and recovering the protein from the culture are summarized, for example, in standard laboratory manuals, such as those published by Cold Spring Harbor Laboratories, Cold Spring Harbor, NY.

Thus, for recombinant production of the hybrid cytokines, suitably constructed DNA encoding the desired hybrid is operably linked to control sequences in a suitable expression system which is then transformed or transfected into a compatible host. The host cells are cultured using conditions appropriate to their growth, and expression is preferably induced after some growth has occurred. Production of the hybrid cytokine is then monitored and the cytokine collected from the culture either from the supernatant or by lysing the cells.

Purification procedures analogous to those known in the art for the native cytokines can be used to effect purification of the cytokine to a form suitable for therapeutic or diagnostic use.

Preparation of Antibodies

Antibodies specifically reactive with the hybrid cytokines of the invention or immunoreactive fragments of these antibodies may be prepared using standard immunization protocols. These may be utilized as polyclonal antisera or the spleen cells or peripheral blood lymphocytes of the immunized animals may be immortalized to obtain isolated cell cultures which produce monoclonal antibodies specific for these hybrids. The antibodies may be used intact, or as fragments such as Fab, Fab' or F(ab')<sub>2</sub> fragments. As the hybrid cytokines are relatively large proteins, it should not be necessary to enhance their immunogenicity by conjugation to carrier; however, such enhancement is possible and construction of such conjugates is well known in the art.

Thus, the hybrid cytokine, optionally conjugated to an immunological carrier, is administered in a standard immunization protocol with or without the use of adjuvant to a suitable subject, usually rats, sheep, or rabbits. Antibody formation is monitored by titrating the serum using the cytokine as antigen and employing standard immunoassay techniques. When high titers are achieved, the sera can be used per se or the spleen cells or peripheral blood lymphocytes isolated and immortalized, for example, using the fusion technique of Kohler and Millstein to provide immortalized cells capable of secreting the desired monoclonal antibodies. Individual clones of these immortalized cells are then screened, again using standard immunological techniques, for those colonies which secrete antibodies specifically immunoreactive with the hybrid cytokine immunogen.

The antibodies prepared in the foregoing manner or fragments thereof are useful in diagnostic assays for monitoring the pharmacokinetics and progress of therapeutic regimens using the hybrid cytokines of the invention. Thus, the dosage levels of the hybrid cytokines in the therapeutic applications set forth below can be regulated according to the metabolic fate of the previously administered dosages.

#### Administration and Utility

The hybrid cytokines of the invention are useful in treating the indications for which their native counterparts are often employed. However, the hybrid forms of the cytokines possess unique properties which make them suitable alternatives in the methods and procedures commonly employed with respect to the native molecules.

In addition, some of the hybrid cytokines are capable of binding the receptors ordinarily bound by the native molecules but fail to activate these receptors. These forms of the hybrid cytokines are, thus, antagonists. These may be useful in treating conditions where presence of the parent factor that ordinarily binds to the receptor is responsible for undesired cell proliferation. For example, IL-6 and OSM are known to be associated in high levels with Kaposi's sarcoma. These are found also in high concentrations in the synovial fluid from patients suffering from rheumatoid arthritis. In these conditions, the hybrid cytokine antagonists are particularly useful.

Conversely, the hybrid cytokines which are agonists can be employed in circumstances wherein the native cytokines are often used. For instance, these agonist hybrid cytokines may be used in liver cell regeneration and in *in vitro* fertilization procedures to enhance these processes.

The hybrid cytokine may possess properties exhibited by neither of its components taken alone. It is known, for example, that coadministration of LIE and G-CSF results in a synergistic effect in inhibiting colony formation and inducing differentiation of human U937 and HL60 myelocytic leukemia cell lines although neither alone has this effect (Maekawa, T., and Metcalf, D., *Leukemia* (1989) 3:270-276.) Similarly, applicants have found that although neither LIP nor OSM inhibit colony formation of U937, when supplied in combination, at 10 ng/ml using 300 cells in soft agar, more than 60% inhibition of colony formation is obtained.

Thus, combination of the  $\alpha$ -helical regions from more than one growth factor results in hybrid cytokines with a unique spectrum of properties. These hybrid cytokines are useful generally in inhibiting tumor proliferation, in bone remodeling, in stimulating the differentiation and growth of desired cells, such as neurons or T-cells, and in enhancing the differentiation of hematopoietic cells. These factors are therefore highly useful in the direct treatment in the malignancies. They are especially useful in maintaining the general health and immune capacity of a subject undergoing radiation therapy or chemotherapy for such indications.

The selection of particular conditions or procedures suitable for the hybrid cytokine in question depends, of course, on its particular spectrum of agonist or antagonist activities.

The properties of a particular hybrid can be ascertained through standard *in vitro* tests well known in the art. Such tests include those, for example, which show induction of differentiation into macrophages (Tomita, M., et al., *J Biol Chem* (1984) 259:10978-10982); ability to enhance interleukin-3-dependent colony formation of primitive blast cells (Leary, A.G., et al., *Blood* (1990) 75:1960-1964); promotion of megakaryocyte growth and differentiation (Metcalf, D., et al., *Blood* (1990) 76:50-56); induction of neuronal differentiation (Yamamuri, T., et al., *Science* (1989) 246:1412-1416); and induction of bone resorption (Ishimi, Y., et al., *J Immunol* (1990) 145:3297-3303). A large number of indicators *in vitro* of the ability of these factors to stimulate growth and differentiation of desired cells and inhibit the growth of undesired malignant cells is known in the art. Animal model systems can also be used to verify the unique spectrum of properties associated with each hybrid cytokine.

Particularly useful *in vitro* tests which can be used to confirm the spectrum of activity of the hybrid cytokines are as follows:

The inhibition of DNA synthesis in M-1 myeloid leukemic cells can be measured; the effect on growth of human A-375 melanoma cells (Zarling, J.M. et al., *Proc Natl Acad Sci USA* (1986) 83:9739-9743) may be measured, or the effect of these factors on embryonic stem cells cultured *in vitro* as described by Smith, A.G. et al., *Devel Biol* (1987) 121:1-9; Williams, R.L. et al., *Nature* (1988) 336:684-687, can be determined.

The foregoing procedures can be adapted to assess both agonist and antagonist behavior. In assessing antagonist behavior, the candidate hybrid cytokine is used in the presence of a known agonist and its effect on the activity of the known agonist is assessed.

As set forth above, the hybrid cytokines of the invention are applicable to *in vivo* and *in vitro* procedures involving both human and animal cells. They are suitable for both medical and veterinary use.

For therapeutic use, the hybrid cytokines of the invention are formulated into standard pharmaceutical compositions suitable for the administration of proteins. Suitable formulations can be found, for example, in *Remington's Pharmaceutical Sciences*, latest edition, Mack Publishing Company, Easton, PA. Comparable compositions for veterinary use are also known in the art. Generally, administration is systemic, usually by injection, such as intravenous or intramuscular injection or can be effected by transdermal or preferably transmucosal delivery. Suitable formulations for effecting



transmucosal delivery include, for example, various detergents and bile salts or fusidic acid derivatives. Enteric compositions which permit oral administration may also be employed.

The dosage levels of the hybrid cytokines of the invention are comparable to those useful for the native molecules. These levels are understood in the art, and the precise dosage can be adjusted according to the condition of the patient, the mode of administration, and the judgment of the attending physician.

The hybrid cytokines of the invention may also be labeled using suitable fluorometric, colorimetric, enzymic, or radioactive labels for use in assays to ascertain the formation of antibodies in patients being treated.

# SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: Todaro, George J.  
Rose, Timothy M.

(ii) TITLE OF INVENTION: HYBRID CYTOKINES

(iii) NUMBER OF SEQUENCES: 8

## (iv) CORRESPONDENCE ADDRESS:

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## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/753,178  
(B) FILING DATE: 30-AUG-1991  
(C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Dr. Volker Vossius

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## (2) INFORMATION FOR SEQ ID NO:1:

### (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 202 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

1 Met Lys Val Leu Ala Ala Gly Val Val Pro Leu Leu Leu Val Leu His  
 5 10 15  
 20 Trp Lys His Gly Ala Gly Ser Pro Leu Pro Ile Thr Pro Val Asn Ala  
 25 30  
 35 Thr Cys Ala Ile Arg His Pro Cys His Asn Asn Leu Met Asn Gln Ile  
 40 45  
 50 Arg Ser Gln Leu Ala Gln Leu Asn Gly Ser Ala Asn Ala Leu Phe Ile  
 55 60  
 65 Leu Tyr Tyr Thr Ala Gln Gly Glu Pro Phe Pro Asn Asn Leu Asp Lys  
 70 75 80  
 85 Leu Cys Gly Pro Asn Val Thr Asp Phe Pro Pro Phe His Ala Asn Gly  
 90 95  
 100 Thr Glu Lys Ala Lys Leu Val Glu Leu Tyr Arg Ile Val Val Tyr Leu  
 105 110  
 115 Gly Thr Ser Leu Gly Asn Ile Thr Arg Asp Gln Lys Ile Leu Asn Pro  
 120 125  
 130 Ser Ala Leu Ser Leu His Ser Lys Leu Asn Ala Thr Ala Asp Ile Leu  
 135 140  
 145 Arg Gly Leu Leu Ser Asn Val Leu Cys Arg Leu Cys Ser Lys Tyr His  
 150 155 160  
 165 Val Gly His Val Asp Val Thr Tyr Gly Pro Asp Thr Ser Gly Lys Asp  
 170 175  
 180 Val Phe Gln Lys Lys Lys Leu Gly Cys Gln Leu Leu Gly Lys Tyr Lys  
 185 190  
 195 Gln Ile Ile Ala Val Leu Ala Gln Ala Phe  
 200

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Lys Val Leu Ala Ala Gly Ile Val Pro Leu Leu Leu Leu Val Leu  
 1 5 10 15  
 5 His Trp Lys His Gly Ala Gly Ser Pro Leu Pro Ile Thr Pro Val Asn  
 20 25 30  
 Ala Thr Cys Ala Ile Arg His Pro Cys His Gly Asn Leu Met Asn Gln  
 35 40 45  
 10 Ile Lys Asn Gln Leu Ala Gln Leu Asn Gly Ser Ala Asn Ala Leu Phe  
 50 55 60  
 Ile Ser Tyr Tyr Thr Ala Gln Gly Glu Pro Phe Pro Asn Asn Val Glu  
 65 70 75 80  
 Lys Leu Cys Ala Pro Asn Met Thr Asp Phe Pro Ser Phe His Gly Asn  
 85 90 95  
 20 Gly Thr Glu Lys Thr Lys Leu Val Glu Leu Tyr Arg Met Val Ala Tyr  
 100 105 110  
 Leu Ser Ala Ser Leu Thr Asn Ile Thr Arg Asp Gln Lys Val Leu Asn  
 115 120 125  
 25 Pro Thr Ala Val Ser Leu Gln Val Lys Leu Asn Ala Thr Ile Asp Val  
 130 135 140  
 Met Arg Gly Leu Leu Ser Asn Val Leu Cys Arg Leu Cys Asn Lys Tyr  
 145 150 155 160  
 Arg Val Gly His Val Asp Val Pro Pro Val Pro Asp His Ser Asp Lys  
 165 170 175  
 35 Glu Ala Phe Gln Arg Lys Lys Leu Gly Cys Gln Leu Leu Gly Thr Tyr  
 180 185 190  
 Lys Gln Val Ile Ser Val Val Val Gln Ala Phe  
 195 200  
 40

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala  
 1 5 10 15  
 Leu Leu Phe Pro Ser Met Ala Ser Met Ala Ala Ile Gly Ser Cys Ser  
 20 25 30  
 Lys Glu Tyr Arg Val Leu Leu Gly Gln Leu Gln Lys Gln Thr Asp Leu  
 35 40 45  
 Met Gln Asp Thr Ser Arg Leu Leu Asp Pro Tyr Ile Arg Ile Gln Gly  
 50 55 60  
 Leu Asp Val Pro Lys Leu Arg Glu His Cys Arg Glu Arg Pro Gly Ala  
 65 70 75 80  
 Phe Pro Ser Glu Glu Thr Leu Arg Gly Leu Gly Arg Arg Gly Phe Leu  
 85 90 95  
 Gln Thr Leu Asn Ala Thr Leu Gly Cys Val Leu His Arg Leu Ala Asp  
 100 105 110  
 Leu Glu Gln Arg Leu Pro Lys Ala Gln Asp Leu Glu Arg Ser Gly Leu  
 115 120 125  
 Asn Ile Glu Asp Leu Glu Lys Leu Gln Met Ala Arg Pro Asn Ile Leu  
 130 135 140  
 Gly Leu Arg Asn Asn Ile Tyr Cys Met Ala Gln Leu Leu Asp Asn Ser  
 145 150 155 160  
 Asp Thr Ala Glu Pro Thr Lys Ala Gly Arg Gly Ala Ser Gln Pro Pro  
 165 170 175  
 Thr Pro Thr Pro Ala Ser Asp Ala Phe Gln Arg Lys Leu Glu Gly Cys  
 180 185 190  
 Arg Phe Leu His Gly Tyr His Arg Phe Met His Ser Val Gly Arg Val  
 195 200 205  
 Phe Ser Lys Trp Gly Glu Ser Pro Asn Arg Ser Arg Arg His Ser Pro  
 210 215 220  
 His Gln Ala Leu Arg Lys Gly Val Arg Arg Thr Arg Pro Ser Arg Lys  
 225 230 235 240  
 Gly Lys Arg Leu Met Thr Arg Gly Gln Leu Pro Arg  
 245 250

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

5           Gln Thr Asp Leu Met Gln Asp Thr Ser Arg Leu Leu Asp Pro Tyr Ile  
           1                   5                   10                   15  
           Arg Ile Gln Gly Leu Asp Ile Pro Lys Leu Arg Glu His Cys Arg Glu  
                   20                   25                   30  
 10           Arg Pro Gly Ala Phe Pro Ser Glu Glu Thr Leu Arg Gly Leu Gly Arg  
                   35                   40                   45  
           Arg Gly Phe Leu Gln Thr Leu Asn Asp Thr Leu Gly Cys Val Leu His  
                   50                   55                   60  
 15           Arg Leu Ala Asp Leu Glu Gln His Leu Pro Lys Ala Gln Asp Leu Glu  
                   65                   70                   75                   80  
 20           Arg Ser Gly Leu Asn Ile Glu Asp Leu Glu Lys Leu Gln Met Ala Arg  
                   85                   90                   95  
           Pro Asn Val Leu Gly Leu Arg Asn Asn Ile Tyr Cys Met Ala Gln Leu  
                   100                   105                   110  
 25           Leu Asp Asn Ser Asp Met Thr Glu Pro Thr Lys Ala Gly Arg Gly Ala  
                   115                   120                   125  
           Ser Gln Pro Pro Thr Pro Thr Pro Thr Ser Asp Val Phe Gln Arg Lys  
                   130                   135                   140  
           Leu Glu Gly Cys Ser Phe Leu His Gly Tyr His Arg Phe Met His Ser  
                   145                   150                   155                   160  
 35           Val Gly Gln Val Phe Ser Lys Trp Gly Glu Ser Pro Asn Arg Ser Arg  
                   165                   170                   175  
           Arg His Ser Pro His Gln Ala Leu Arg Lys Gly Val Arg Arg Thr Arg  
                   180                   185                   190  
 40           Pro Ser Arg Lys Gly Asn Arg Leu Met Thr Arg Gly Gln Leu  
                   195                   200                   205

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

1 Met Ala Gly Pro Ala Thr Gln Ser Pro Met Lys Leu Met Ala Leu Gln  
 5 5 10 15  
 5 Leu Leu Leu Trp His Ser Ala Leu Trp Thr Val Gln Glu Ala Thr Pro  
 20 25 30  
 10 Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Cys Leu  
 35 40 45  
 Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys  
 50 55 60  
 15 Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu  
 65 70 75 80  
 Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser  
 85 90 95  
 20 Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu  
 100 105 110  
 Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu  
 115 120 125  
 25 Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala  
 130 135 140  
 30 Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu  
 145 150 155 160  
 Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg  
 165 170 175  
 35 Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu  
 180 185 190  
 40 Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro  
 195 200

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ala Gln Leu Ser Ala Gln Arg Arg Met Lys Leu Met Ala Leu Gln  
 1 5 10 15  
 5 Leu Leu Leu Trp Gln Ser Ala Leu Trp Ser Gly Arg Glu Ala Val Pro  
 20 25 30  
 Leu Val Thr Val Ser Ala Leu Pro Pro Ser Leu Pro Leu Pro Arg Ser  
 35 40 45  
 10 Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Ala Ser Gly  
 50 55 60  
 Ser Val Leu Leu Glu Gln Leu Cys Ala Thr Tyr Lys Leu Cys His Pro  
 65 70 75 80  
 Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Lys Ala Ser  
 85 90 95  
 20 Leu Ser Gly Cys Ser Ser Gln Ala Leu Gln Gln Thr Gln Cys Leu Ser  
 100 105 110  
 Gln Leu His Ser Gly Leu Cys Leu Tyr Gln Gly Leu Leu Gln Ala Leu  
 115 120 125  
 25 Ser Gly Ile Ser Pro Ala Leu Ala Pro Thr Leu Asp Leu Leu Gln Leu  
 130 135 140  
 Asp Val Ala Asn Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Asn Leu  
 145 150 155 160  
 Gly Val Ala Pro Thr Val Gln Pro Thr Gln Ser Ala Met Pro Ala Phe  
 165 170 175  
 35 Thr Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Ala Ile Ser Tyr  
 180 185 190  
 Leu Gln Gly Phe Leu Glu Thr Ala Arg Leu Ala Leu His His Leu Ala  
 195 200 205  
 40

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Asn Ser Phe Ser Thr Ser Ala Phe Gly Pro Val Ala Phe Ser Leu  
 1 5 10 15  
 Gly Leu Leu Leu Val Leu Pro Ala Ala Phe Pro Ala Pro Val Pro Pro  
 20 25 30  
 Gly Glu Asp Ser Lys Asp Val Ala Ala Pro His Arg Gln Pro Leu Thr  
 35 40 45  
 Ser Ser Glu Arg Ile Asp Lys Gln Ile Arg Tyr Ile Leu Asp Gly Ile  
 50 55 60  
 Ser Ala Leu Arg Lys Glu Thr Cys Asn Lys Ser Asn Met Cys Glu Ser  
 65 70 75 80  
 Ser Lys Glu Ala Leu Ala Glu Asn Asn Leu Asn Leu Pro Lys Met Ala  
 85 90 95  
 Glu Lys Asp Gly Cys Phe Gln Ser Gly Phe Asn Glu Glu Thr Cys Leu  
 100 105 110  
 Val Lys Ile Ile Thr Gly Leu Leu Glu Phe Glu Val Tyr Leu Glu Tyr  
 115 120 125  
 Leu Gln Asn Arg Phe Glu Ser Ser Glu Glu Gln Ala Arg Ala Val Gln  
 130 135 140  
 Met Ser Thr Lys Val Leu Ile Gln Phe Leu Gln Lys Lys Ala Lys Asn  
 145 150 155 160  
 Leu Asp Ala Ile Thr Thr Pro Asp Pro Thr Thr Asn Ala Ser Leu Leu  
 165 170 175  
 Thr Lys Leu Gln Ala Gln Asn Gln Trp Leu Gln Asp Met Thr Thr His  
 180 185 190  
 Leu Ile Leu Arg Ser Phe Lys Glu Phe Leu Gln Ser Ser Leu Arg Ala  
 195 200 205  
 Leu Arg Gln Met  
 210

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:



Met Lys Phe Leu Ser Ala Arg Asp Phe His Pro Val Ala Phe Leu Gly  
 1 5 10 15  
 5 Leu Met Leu Val Thr Thr Thr Ala Phe Pro Thr Ser Gln Val Arg Arg  
 20 25 30  
 Gly Asp Phe Thr Glu Asp Thr Thr Pro Asn Arg Pro Val Tyr Thr Thr  
 35 40 45  
 10 Ser Gln Val Gly Gly Leu Ile Thr His Val Leu Trp Glu Ile Val Glu  
 50 55 60  
 Met Arg Lys Glu Leu Cys Asn Gly Asn Ser Asp Cys Met Asn Asn Asp  
 65 70 75 80  
 Asp Ala Leu Ala Glu Asn Asn Leu Lys Leu Pro Glu Ile Gln Arg Asn  
 85 90 95  
 20 Asp Gly Cys Tyr Gln Thr Gly Tyr Asn Gln Glu Ile Cys Leu Leu Lys  
 100 105 110  
 Ile Ser Ser Gly Leu Leu Glu Tyr His Ser Tyr Leu Glu Tyr Met Lys  
 115 120 125  
 25 Asn Asn Leu Lys Asp Asn Lys Lys Asp Lys Ala Arg Val Leu Gln Arg  
 130 135 140  
 Asp Thr Glu Thr Leu Ile His Ile Phe Asn Gln Glu Val Lys Asp Leu  
 145 150 155 160  
 His Lys Ile Val Leu Pro Thr Pro Ile Ser Asn Ala Leu Leu Thr Asp  
 165 170 175  
 35 Lys Leu Glu Ser Gln Lys Glu Trp Leu Arg Thr Lys Thr Ile Gln Phe  
 180 185 190  
 Ile Leu Lys Ser Leu Glu Glu Phe Leu Lys Val Thr Leu Arg Ser Thr  
 195 200 205  
 40 Arg Gln Thr  
 210  
 45

#### Claims

1. A hybrid cytokine comprising a first, second, third and fourth  $\alpha$ -helical region wherein each of said first, second, third and fourth  $\alpha$ -helical regions is derived from the corresponding  $\alpha$ -helical region of a factor selected from the group consisting of leukemia inhibitory factor (LIF or L), granulocyte-colony stimulating factor (G-CSF or G), interleukin-6 (IL-6 or I), and oncostatin-M (OSM or O); and

wherein at least one said  $\alpha$ -helical region of said cytokine is derived from a factor different from that from which at least one additional region of said cytokine is derived.
2. The hybrid cytokine of claim 1 which is GGLL; GGII; GGGO; GILO; LOGI; LLGG; IIGG; OOGG; LLJI; GGGI; OOOI; LLLI; IIII; GGGO; OOOG; LLLO; IIII; GGGL; OOOI; LLLG; IIIL; IGGG; IOOO; ILLL; OIII; OGGG; or GOOO; or which further contains, between each of said first, second, third and fourth  $\alpha$ -helical regions linking regions of 5-100 amino acids.

3. The cytokine of claims 2 or 14 wherein each of said linking regions is independently derived from a corresponding linking region of LIF, G-CSF, IL-6 or OSM, or  
 wherein each of said linking regions between said first and second, and between said third and fourth  $\alpha$ -helical region is selected so as to result in an anti-polar orientation of said first and fourth  $\alpha$ -helical region.
4. The hybrid cytokine of claim 3 wherein the linking regions between said first and second and said third and fourth  $\alpha$ -helical regions are each 20-100 amino acids, or  
 wherein each of the linking regions between said first and second and said third and fourth  $\alpha$ -helical regions are each less than 20 amino acids; or  
 wherein each of said linking regions between said first and second and said third and fourth  $\alpha$ -helical regions are either both derived from OSM and/or LIF or both derived from G-CSF and/or IL-6.
5. The cytokine of claim 3 which is selected from the group consisting of GIGILIL; GIGgIII; GgGgOgO; GiGiGol; liGgGgG; GgliLiO; LgOgGgl; GgGgGgO; GgGgGgL; OoOoOoG; LILILIG; GoOoOoO; OgGgGgG; LgGgGgG; GiG-gGil; and LoLlloI.
6. The cytokine of anyone of claims 1 to 5 or 14, wherein each said corresponding region is human, or which is conjugated to label.
7. A recombinant DNA that encodes the hybrid cytokine of anyone of claims 1 to 6 or 14.
8. An expression system capable, when contained in a recombinant host cell, of effecting the expression of a DNA encoding the hybrid cytokine of anyone of claims 1 to 6 or 14, wherein said expression system comprises said encoding DNA operably linked to control sequences compatible with said host.
9. Recombinant host cells transformed with the expression system of claim 8.
10. A method to produce a hybrid cytokine protein comprising a first, second, third and fourth  $\alpha$ -helical region wherein each of said first, second, third and fourth  $\alpha$ -helical regions is derived from the corresponding  $\alpha$ -helical region of a factor selected from the group consisting of leukemia inhibitory factor (LIF), granulocyte-colony stimulating factor (G-CSF), interleukin-6 (IL-6), and oncostatin-M (OSM); and  
 wherein at least one said  $\alpha$ -helical region of said cytokine is derived from a factor different from that from which at least one additional region of said cytokine is derived, which method comprises culturing the recombinant host cells of claim 9 under conditions which effect the expression of said encoding DNA; and recovering said hybrid cytokine from the culture.
11. A pharmaceutical or veterinary composition useful in affecting the proliferation and/or differentiation of target cells which composition comprises an effective amount of the hybrid cytokine of anyone of claims 1 to 6 or 14 in a mixture with at least one pharmaceutically acceptable excipient.
12. Antibodies or fragments thereof specifically immunoreactive with the hybrid cytokine of anyone of claims 1 to 6 or 14.
13. A method to prepare a hybrid cytokine useful in therapy which method comprises:  
 preparing a candidate cytokine comprising a first, second, third and fourth  $\alpha$ -helical region wherein each of said first, second, third and fourth  $\alpha$ -helical regions is derived from the corresponding  $\alpha$ -helical region of a factor selected from the group consisting of LIF, G-CSF, IL-6 and OSM;  
 wherein at least one said  $\alpha$ -helical region of said cytokine is derived from a factor different from that from which at least one additional region of the cytokine is derived, to obtain a candidate hybrid cytokine; and testing said candidate cytokine in an *in vitro* assay system for ability to affect the growth of target cells; and selecting a cytokine which provides the desired effect.
14. The cytokine of claim 1 which is  
 GGGI; OOOI; LLLI; IIII; GGGO; OOOO; LLLO; IIIG; GGGL; OOOL; LLLG; IIIL; IGGG; IOOO; ILLL; OIII; OGGG; GGOO; OLLL; GIII; LGGG; LOOO; GLLL; LIII; GGLL; GGII; GGOO; GILO; LOGI; LLII; LLGG; IIGG; and OOGG

which further contains, between each of said first, second, third and fourth  $\alpha$ -helical regions linking regions of 5-100 amino acids.

## 5 Patentansprüche

1. Ein hybrides Cytokin, umfassend einen ersten, zweiten, dritten und vierten  $\alpha$ -helikalen Bereich, wobei jeder der ersten, zweiten, dritten und vierten  $\alpha$ -helikalen Bereiche von dem entsprechenden  $\alpha$ -helikalen Bereich eines Faktors abgeleitet ist, der ausgewählt ist aus der Gruppe bestehend aus Leukämie-inhibierender Faktor (LIF oder L), Granulozyten-Kolonie-stimulierender Faktor (G-CSF oder G, Interleukin-6 (IL-6 oder I) und Onkostatin-M (OSM oder O), und wobei mindestens ein  $\alpha$ -helikaler Bereich des Cytokins von einem Faktor abgeleitet ist, der von dem Faktor verschieden ist, von dem mindestens ein zusätzlicher Bereich des Cytokins abgeleitet ist.
2. Das hybride Cytokin nach Anspruch 1, das GGLL, GGII, GGOO, GILO, LOGI, LLGG, IIGG, OOGG, LLII, GGGI, OOOI, LLLI, IIIO, GGGO, OOOO, LLLO, IIIG, GGGL, OOOO, LLLG, IIIL, IGGG, IOOO, ILLL, OIII, OGGG oder GOOO ist, oder das ferner zwischen jedem der ersten, zweiten, dritten und vierten  $\alpha$ -helikalen Bereiche Verbindungsbereiche von 5 bis 100 Aminosäuren enthält.
3. Das Cytokin nach Anspruch 2 oder 14, wobei jeder der Verbindungsbereiche unabhängig voneinander von einem entsprechenden Verbindungsbereich von LIF, G-CSF, IL-6 oder OSM abgeleitet ist, oder wobei jeder der Verbindungsbereiche zwischen dem ersten und zweiten und zwischen dem dritten und vierten  $\alpha$ -helikalen Bereich so ausgewählt ist, daß sich eine antipolare Orientierung des ersten und vierten  $\alpha$ -helikalen Bereichs ergibt.
4. Das hybride Cytokin nach Anspruch 3, wobei die Verbindungsbereiche zwischen dem ersten und zweiten und dem dritten und vierten  $\alpha$ -helikalen Bereich jeweils 20 bis 100 Aminosäuren betragen oder wobei jeder der Verbindungsbereiche zwischen den ersten und zweiten und den dritten und vierten  $\alpha$ -helikalen Bereichen jeweils weniger als 20 Aminosäuren beträgt, oder wobei jeder der Verbindungsbereiche zwischen den ersten und zweiten und den dritten und vierten  $\alpha$ -helikalen Bereichen entweder jeweils von OSM und/oder LIF oder von G-CSF und/oder IL-6 abgeleitet ist.
5. Das Cytokin nach Anspruch 3, das aus der Gruppe ausgewählt ist bestehend aus GIGILIL, GIGgIII, GGGgOgO, GIGiGol, IIGgGgG, GgIIiLiO, LgOgGgI, GgGgGgO, GgGgGgL, OoOoOoG, LILILIG, GoOoOoO, OgGgGgG, LgGgGgG, GiGgGil und LoLlIol.
6. Das Cytokin nach einem der Ansprüche 1 bis 5 oder 14, wobei jeder entsprechende Bereich vom Menschen abgeleitet ist oder an eine Markierung gekoppelt ist.
7. Eine rekombinante DNA, die das hybride Cytokin nach einem der Ansprüche 1 bis 6 oder 14 kodiert.
8. Ein Expressionssystem, das in einer rekombinanten Wirtszelle fähig ist, die Expression einer DNA zu bewirken, die das hybride Cytokin nach einem der Ansprüche 1 bis 6 oder 14 kodiert, wobei das Expressionssystem die kodierende DNA umfaßt, die operativ mit Kontroll-sequenzen verbunden ist, die mit dem Wirt kompatibel sind.
9. Rekombinante Wirtszellen, die mit dem Expressionssystem nach Anspruch 8 transformiert sind.
10. Ein Verfahren zur Herstellung eines hybriden Cytokin-Proteins, umfassend einen ersten, zweiten, dritten und vierten  $\alpha$ -helikalen Bereich, wobei jeder der ersten, zweiten, dritten und vierten  $\alpha$ -helikalen Bereiche von dem entsprechenden  $\alpha$ -helikalen Bereich eines Faktors abgeleitet ist, der ausgewählt ist aus der Gruppe bestehend aus Leukämie-inhibierender Faktor (LIF), Granulozyten-Kolonie-stimulierender Faktor (G-CSF), Interleukin 6 (IL-6) und Onkostatin-M (OSM), und wobei mindestens ein  $\alpha$ -helikaler Bereich des Cytokins von einem Faktor abgeleitet ist, der von dem Faktor verschieden ist, von dem mindestens ein zusätzlicher Bereich des Cytokins abgeleitet ist, wobei das Verfahren das Kultivieren der rekombinanten Wirtszellen nach Anspruch 9 unter Bedingungen umfaßt, die die Expression der kodierenden DNA bewirken, und das hybride Cytokin aus der Kultur isoliert wird.
11. Eine pharmazeutische oder veterinärmedizinische Zusammensetzung, verwendbar zur Beeinflussung der Proliferation und/oder Differenzierung von Zielzellen, wobei die Zusammensetzung eine wirksame Menge des hybriden Cytokins nach einem der Ansprüche 1 bis 6 oder 14 in einem Gemisch mit mindestens einer pharmazeutisch verträglichen Trägersubstanz umfaßt.

12. Antikörper oder deren Fragmente, die spezifisch mit dem hybriden Cytokin nach einem der Ansprüche 1 bis 6 oder 14 immunreaktiv sind.

13. Ein Verfahren zur Herstellung eines hybriden Cytokins zur Therapie, wobei das Verfahren umfaßt:

Herstellen eines Cytokins als Kandidat, umfassend einen ersten, zweiten, dritten und vierten  $\alpha$ -helikalen Bereich, wobei jeder der ersten, zweiten, dritten und vierten  $\alpha$ -helikalen Bereiche abgeleitet ist von dem entsprechenden  $\alpha$ -helikalen Bereich eines Faktors, ausgewählt aus der Gruppe bestehend aus LIF, F-CSF, IL-6 und OSM, wobei mindestens ein  $\alpha$ -helikaler Bereich des Cytokins von einem Faktor abgeleitet ist, der unterschiedlich von einem Faktor ist, von dem mindestens ein weiterer Bereich des Cytokins abgeleitet ist, und

Testen des erhaltenen hybriden Cytokins als Kandidat in einem *in vitro*-Nachweissystem auf die Fähigkeit, das Wachstum von Zielzellen zu beeinflussen, und

Auswählen eines Cytokins, das die gewünschte Wirkung liefert.

14. Das Cytokin nach Anspruch 1, das GGGI, OOOI, LLLI, IIII, GGGO, OOOO, LLLO, IIII, GGGL, OOOO, LLLG, IIII, IGGG, IOOO, ILLL, OIII, OGGG, GOOO, OLLL, GIII, LGGG, LOOO, GLLL, LIII, GLLL, GGII, GGOO, GILO, LOGI, LLII, LLGG, IIGG und OOGG ist, und das ferner zwischen jedem der ersten, zweiten, dritten und vierten  $\alpha$ -helikalen Bereiche Verbindungsbereiche von 5 bis 100 Aminosäuren enthält.

#### Revendications

1. Cytokine hybride comprenant une première, une seconde, une troisième et une quatrième région  $\alpha$ -hélicoïdale, dans laquelle chacune desdites première, deuxième, troisième et quatrième régions  $\alpha$ -hélicoïdales est dérivée de la région  $\alpha$ -hélicoïdale correspondante d'un facteur choisi dans le groupe consistant en le facteur inhibiteur de leucémie (LIF ou L), le facteur de stimulation de colonie de granulocytes (G-CSF ou G), l'interleukine-6 (IL-6 ou I) et l'oncostatine-M (OSM ou O); et où au moins l'une desdites régions  $\alpha$ -hélicoïdales de ladite cytokine est dérivée d'un facteur différent de celui à partir duquel est dérivée au moins une région additionnelle de ladite cytokine.

2. Cytokine hybride selon la revendication 1, qui est GGII, GGII, GGOO, GILO, LOGI, LLGG, IIGG, OOGG, LLII, GGGI, OOOI, LLLI, IIII, GGGO, OOOO, LLLO, IIII, GGGL, OOOO, LLLG, IIII, IGGG, IOOO, ILLL, OIII, OGGG ou GOOO, ou qui contient en outre, entre chacune desdites première, deuxième, troisième et quatrième régions  $\alpha$ -hélicoïdales, des régions de liaison de 5-100 acides aminés.

3. Cytokine selon les revendications 2 ou 14, dans laquelle chacune desdites régions de liaison est dérivée indépendamment d'une région de liaison correspondante de LIF, G-CSF, IL-6 ou OSM, ou dans laquelle chacune desdites régions de liaison entre lesdites première et deuxième et entre lesdites troisième et quatrième régions  $\alpha$ -hélicoïdales est choisie de façon à fournir une orientation anti-polaire desdites première et quatrième régions  $\alpha$ -hélicoïdales.

4. Cytokine hybride selon la revendication 3, dans laquelle les régions de liaison entre lesdites première et deuxième et lesdites troisième et quatrième régions  $\alpha$ -hélicoïdales comportent chacune 20-100 acides aminés; ou

dans laquelle chacune des régions de liaison entre lesdites première et deuxième et lesdites troisième et quatrième régions  $\alpha$ -hélicoïdales ont chacune moins de 20 acides aminés; ou dans laquelle chacune desdites régions de liaison entre lesdites première et deuxième et lesdites troisième et quatrième régions  $\alpha$ -hélicoïdales sont soit toutes deux dérivées d'OSM et/ou de LIF, soit toutes deux dérivées de G-CSF et/ou d'IL-6.

5. Cytokine selon la revendication 3, qui est choisie dans le groupe consistant en GIGIIL, GIGGIII, GgGgOgO, GiGiGoI, IIGgGgG, GgIILiO, LgOgGgI, GgGgGgO, GgGgGgL, OoOoOoG, LILILIG, GoOoOoO, OgGgGgG, LgGgGgG, GiGgGgI, et LoLIloI.

7. ADN recombinant qui code pour la cytokine hybride selon l'une quelconque des revendications 1 à 6 ou 14.

**9. Cellules hôtes recombinantes transformées avec le système d'expression selon la revendication 8.**

et

12. Anticorps ou fragments d'anticorps spécifiquement immunoréactifs avec la cytokine hybride selon l'une quelconque des revendications 1 à 6 ou 14.

la sélection d'une cytokine qui procure l'effet désiré.

G GGI; OOOI; LLLJ; IIIO; GGGO; OOOG; LLLQ; IIIG; GGGL; OOO L; LLLG; IIIL; IGGG; IOOO; ILLL; OIII; OGGG;  
G OOO; OLLL; GIII; LGGG; LOOO; GLLL; LIII; GGLL; GGII; GGOO; GILO; LOGI; LLJI; LLGG; IIGG; et OOGG,  
qui contient en outre, entre chacune desdites première, deuxième, troisième et quatrième régions  $\alpha$ -hélicoïdales,  
des régions de liaison de 5-100 acides aminés.

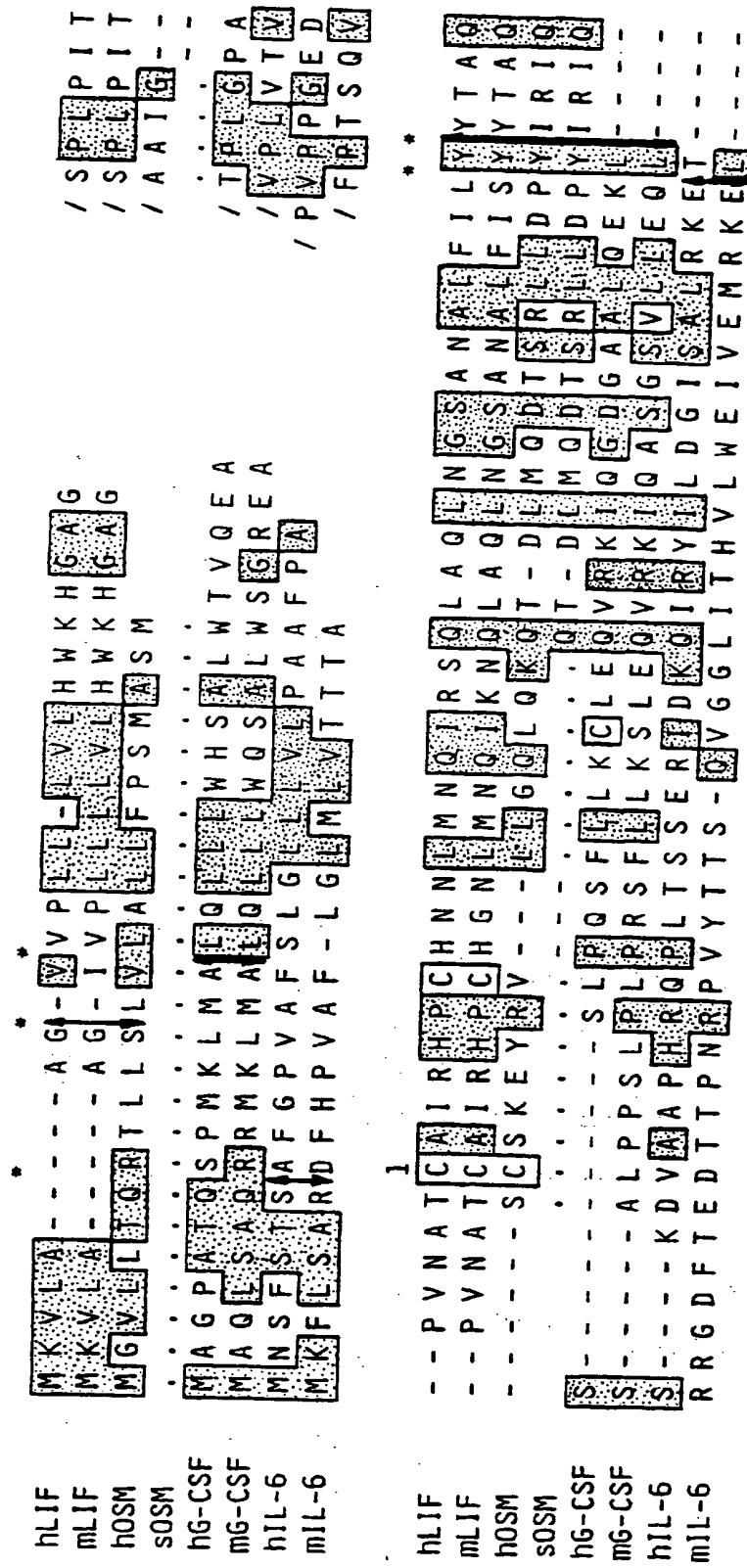
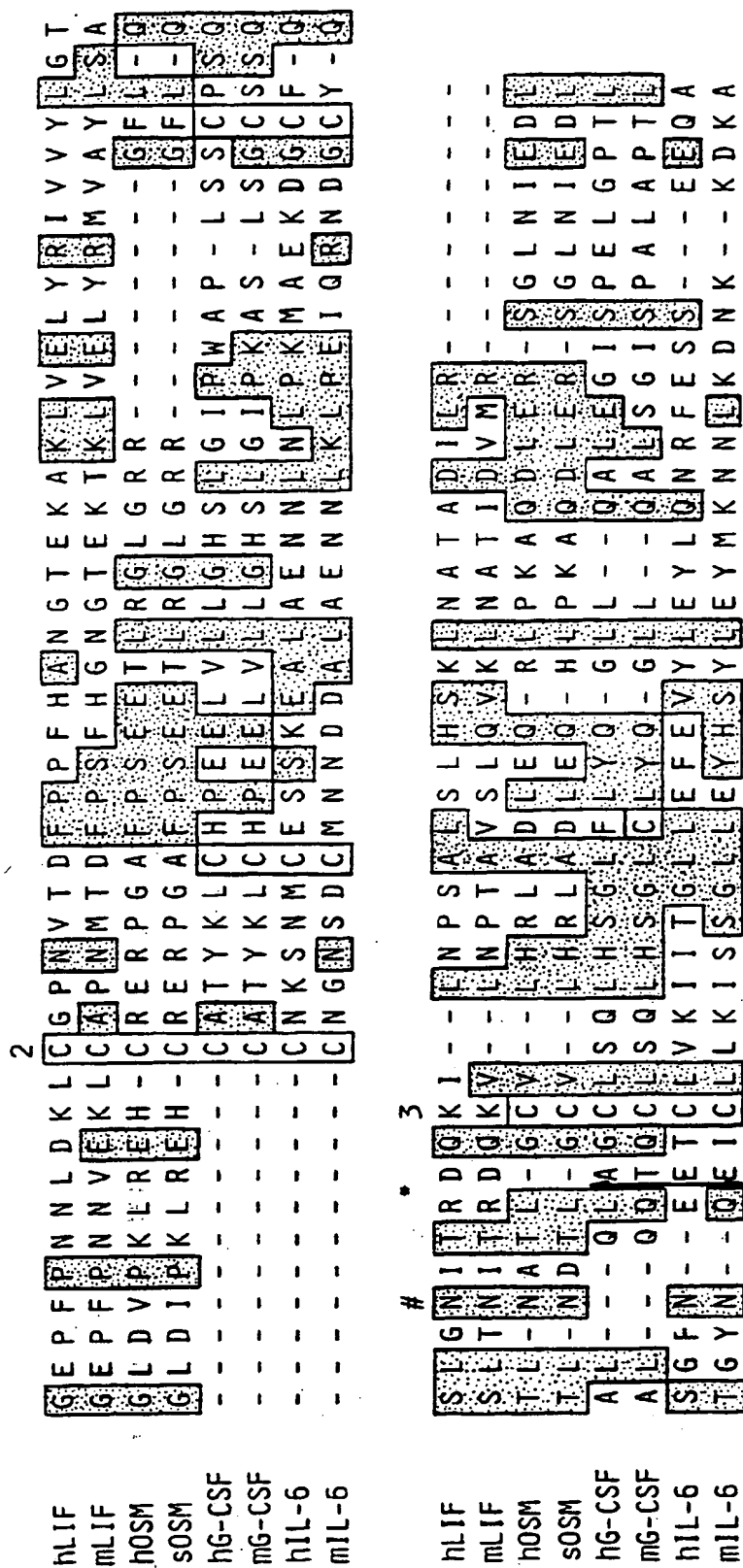


FIG. 1-I



[illegible]

hLIF  
mLIF  
hOSM  
sOSM  
h6-CSF  
mG-CSF  
hIL-6  
mIL-6

hOSM SRR/HSPHQALRKGVRRTRPSRKKGKRLMTRGQLPR  
sOSM SRR/HSPHQALRKGVRRTRPSRKGNRLMTRGQL..

**FIG. 1-3**



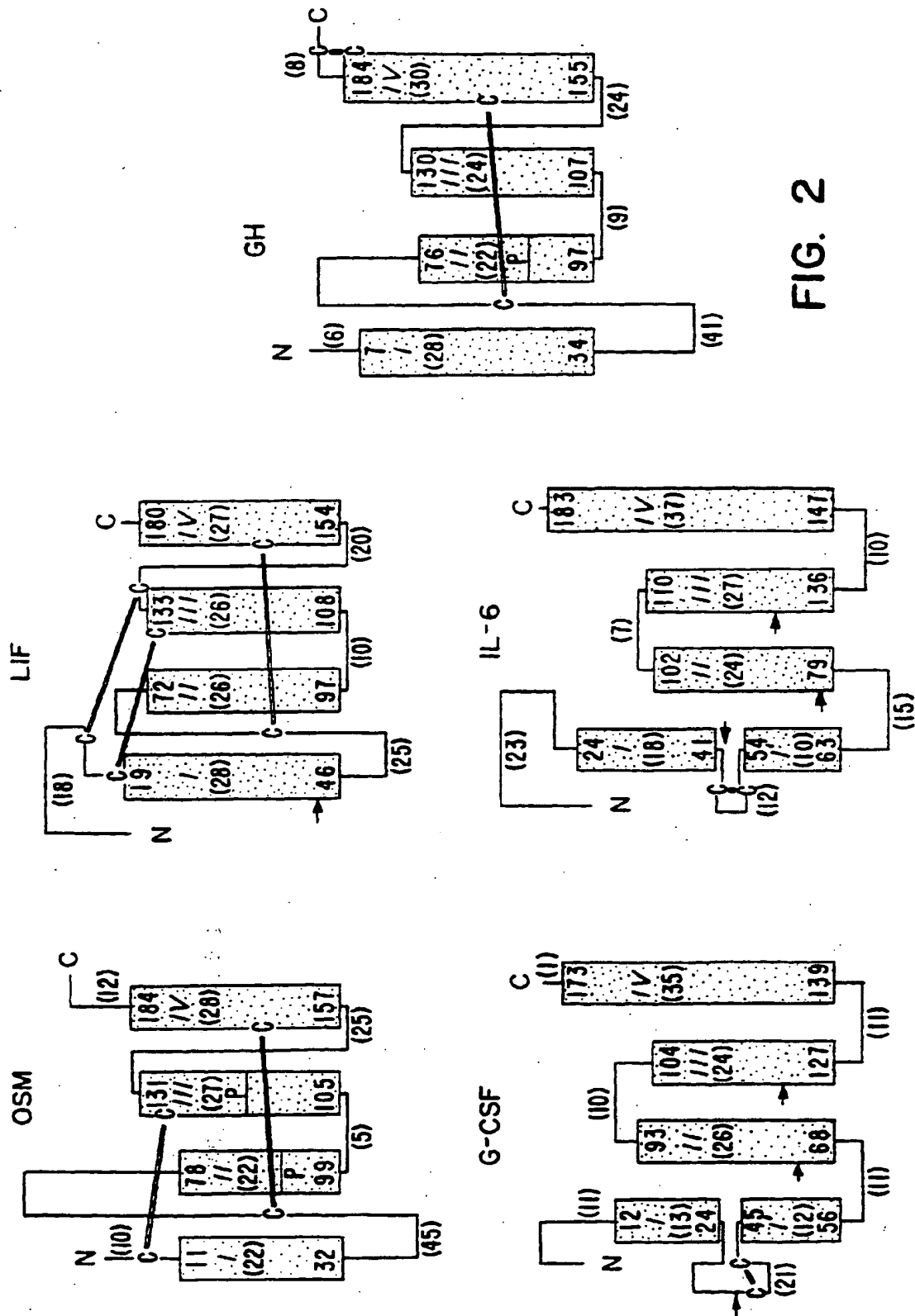


FIG. 2

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